Using Bioinformatics to Efficiently Organize and Analyze Significant Immunogenic Epitope Sequences in Various Stages of *Trypanosoma cruzi*

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The identification of suitable epitope sequences could contribute to finding the right immunogenic element that can offer protection against Chagas disease caused by *Trypanosoma Cruzi* (*T. cruzi*), a protozoan parasite. Due to the complexity of the parasite surface, no vaccine for Chagas disease has been discovered to date. There is an urgent need of an efficient process to identify the most probable surface protein sequences capable of eliciting an immunogenic response. The aim of this project is to use existing bioinformatics tools to computationally filter protein sequences from the *T. cruzi* parasite in order to select the ones that are most likely to contain epitope sequences that stimulate immunological responses from the host. Since this filtering process involves several different steps that require human intervention, we have constructed a Perl script to automate the process. Through mass spectrometry experiments, *T. cruzi* protein sequences were obtained. The epitope prediction software in IEDB (Immune Epitope Database) is one of the primary tools we utilize to filter the sequences and distinguish epitope sequences within the protein. Three different prediction methods, based on artificial neural networks, stabilized matrices, and average relative binding, are used to generate three lists of epitope candidates. We will perform a consensus analysis among these three lists to further improve the confidence level of the predictions. The most likely epitope candidates can then be tested in vitro for immunogenic properties.